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<110> Yaar, Liora
 Alroy, Iris
 Reiss, Yuval
 Taglicht, Daniel N.

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 METHODS

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<400> 5

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 Cys Pro Glu Cys Arg Thr Leu Val Gly Ser Gly Val Glu Glu Leu Pro
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 Ser Asn Ile Leu Leu Val Arg Leu Leu Asp Gly Ile Lys Gln Arg Pro
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 Trp Lys Pro Gly Pro Gly Gly Ser Gly Thr Asn Cys Thr Asn Ala
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 Pro Val Arg Gly Ile Pro Gln Leu Pro Cys Ala Lys Ala Leu Tyr Asn
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 Tyr Glu Gly Lys Glu Pro Gly Asp Leu Lys Phe Ser Lys Gly Asp Ile
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 Asn Gly Ile His Gly Phe Phe Pro Thr Asn Phe Val Gln Ile Ile Lys
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 Pro Leu Pro Gln Pro Pro Pro Gln Cys Lys Ala Leu Tyr Asp Phe Glu
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 Asp Val Leu Thr Val Ile Arg Arg Val Asp Glu Asn Trp Ala Glu Gly
 225 230 235 240
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 Ala Cys Ala Ala Ala Pro Leu Thr Ser Pro Ser Ile Thr Ser Ala
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 Ser Leu Glu Ala Glu Pro Ser Gly Arg Ile Val Thr Val Leu Pro Gly
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 Thr Lys Lys Arg His Ser Phe Thr Ser Leu Thr Met Ala Asn Lys Ser
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 85 90 95
 Ser Gly Leu Ser Cys Ser Ala Pro Ser Gln Val His Ile Ser Thr Thr
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 Gly Leu Ile Val Thr Pro Pro Pro Ser Ser Pro Val Thr Thr Gly Pro
 115 120 125
 Ser Phe Thr Phe Pro Ser Asp Val Pro Tyr Gln Ala Ala Leu Gly Thr
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 405 410 415
 Pro Ser Ile Thr Ser Ala Ser Leu Glu Ala Glu Pro Ser Gly Arg Ile
 420 425 430
 Val Thr Val Leu Pro Gly Leu Pro Thr Ser Pro Asp Ser Ala Ser Ser
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 Ala Cys Gly Asn Ser Ser Ala Thr Lys Pro Asp Lys Asp Ser Lys Lys
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 Glu Lys Lys Gly Leu Leu Lys Leu Leu Ser Gly Ala Ser Thr Lys Arg
 465 470 475 480
 Lys Pro Arg Val Ser Pro Pro Ala Ser Pro Thr Leu Glu Val Glu Leu
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Phe	His	Arg	Lys	Ala	Ser	Ser	Leu	Asp	Ser	Ala	Val	Pro	Ile	Ala	Pro
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Gln	Ser	Glu	Ala	Glu	Leu	Glu	Leu	Lys	Glu	Gly	Asp	Ile	Val	Phe	Val
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His	Lys	Lys	Arg	Glu	Asp	Gly	Trp	Phe	Lys	Gly	Thr	Leu	Gln	Arg	Asn
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 35 40 45
 Cys Pro Glu Cys Arg Thr Leu Val Gly Ser Gly Val Asp Glu Leu Pro
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 Ser Asn Ile Leu Leu Val Arg Leu Leu Asp Gly Ile Lys Gln Arg Pro
 65 70 75 80
 Trp Lys Pro Gly Pro Gly Gly Gly Thr Thr Cys Thr Asn Thr
 85 90 95
 Leu Arg Ala Gln Gly Ser Thr Val Val Asn Cys Gly Ser Lys Asp Leu
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 115 120 125
 Pro Val Arg Gly Ile Pro Gln Leu Pro Cys Ala Lys Ala Leu Tyr Asn
 130 135 140
 Tyr Glu Gly Lys Glu Pro Gly Asp Leu Lys Phe Ser Lys Gly Asp Thr
 145 150 155 160
 Ile Ile Leu Arg Arg Gln Val Asp Glu Asn Trp Tyr His Gly Glu Val
 165 170 175
 Ser Gly Val His Gly Phe Phe Pro Thr Asn Phe Val Gln Ile Ile Lys
 180 185 190
 Pro Leu Pro Gln Pro Pro Gln Cys Lys Ala Leu Tyr Asp Phe Glu
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 Val Lys Asp Lys Glu Ala Asp Lys Asp Cys Leu Pro Phe Ala Lys Asp
 210 215 220
 Asp Val Leu Thr Val Ile Arg Arg Val Asp Glu Asn Trp Ala Glu Gly
 225 230 235 240

Met Leu Ala Asp Lys Ile Gly Ile Phe Pro Ile Ser Tyr Val Glu Phe
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 Asn Ser Ala Ala Lys Gln Leu Ile Glu Trp Asp Lys Pro Pro Val Pro
 260 265 270
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 Phe Thr Ser Leu Thr Met Ala Asn Lys Ser Ser Gln Gly Ser Gln Asn
 305 310 315 320
 Arg His Ser Met Glu Ile Ser Pro Pro Val Leu Ile Ser Ser Ser Asn
 325 330 335
 Pro Thr Ala Ala Ala Arg Ile Ser Glu Leu Ser Gly Leu Ser Cys Ser
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 Ala Pro Ser Gln Val His Ile Ser Thr Thr Gly Leu Ile Val Thr Pro
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 385 390 395 400
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 420 425 430
 Met Gly Pro Arg Pro Val Met Gly Ser Ser Glu Gln Ile Ala His Leu
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 450 455 460
 Pro Arg Lys Glu Asp Glu Leu Glu Leu Arg Lys Gly Glu Met Phe Leu
 465 470 475 480
 Val Phe Glu Arg Cys Gln Asp Gly Trp Tyr Lys Gly Thr Ser Met His
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 Gly Pro Thr Gln Lys Pro Gln Gly Asn Gly Val Ala Gly Asn Pro Ser
 545 550 555 560
 Val Val Pro Thr Ala Val Val Ser Ala Ala His Ile Gln Thr Ser Pro
 565 570 575
 Gln Ala Lys Val Leu Leu His Met Ser Gly Gln Met Thr Val Asn Gln
 580 585 590
 Ala Arg Asn Ala Val Arg Thr Val Ala Ala His Ser Gln Glu Arg Pro
 595 600 605
 Thr Ala Ala Val Thr Pro Ile Gln Val Gln Asn Ala Ala Cys Leu Gly
 610 615 620
 Pro Ala Ser Val Gly Leu Pro His His Ser Leu Ala Ser Gln Pro Leu
 625 630 635 640
 Pro Pro Met Ala Gly Pro Ala Ala His Gly Ala Ala Val Ser Ile Ser
 645 650 655
 Arg Thr Asn Ala Pro Met Ala Cys Ala Ala Gly Ala Ser Leu Ala Ser
 660 665 670
 Pro Asn Met Thr Ser Ala Met Leu Glu Thr Glu Pro Ser Gly Arg Thr
 675 680 685
 Val Thr Ile Leu Pro Gly Leu Pro Thr Ser Pro Glu Ser Ala Ala Ser
 690 695 700

Ala Cys Gly Asn Ser Ser Ala Gly Lys Pro Asp Lys Asp Ser Lys Lys
 705 710 715 720
 Glu Lys Lys Gly Leu Leu Lys Leu Leu Ser Gly Ala Ser Thr Lys Arg
 725 730 735
 Lys Pro Arg Val Ser Pro Pro Ala Ser Pro Thr Leu Asp Val Glu Leu
 740 745 750
 Gly Ala Gly Glu Ala Pro Leu Gln Gly Ala Val Gly Pro Glu Leu Pro
 755 760 765
 Leu Gly Gly Ser His Gly Arg Val Gly Ser Cys Pro Thr Asp Gly Asp
 770 775 780
 Gly Pro Val Ala Ala Gly Thr Ala Ala Leu Ala Gln Asp Ala Phe His
 785 790 795 800
 Arg Lys Thr Ser Ser Leu Asp Ser Ala Val Pro Ile Ala Pro Pro Pro
 805 810 815
 Arg Gln Ala Cys Ser Ser Leu Gly Pro Val Met Asn Glu Ala Arg Pro
 820 825 830
 Val Val Cys Glu Arg His Arg Val Val Val Ser Tyr Pro Pro Gln Ser
 835 840 845
 Glu Ala Glu Leu Glu Leu Lys Glu Gly Asp Ile Val Phe Val His Lys
 850 855 860
 Lys Arg Glu Asp Gly Trp Phe Lys Gly Thr Leu Gln Arg Asn Gly Lys
 865 870 875 880
 Thr Gly Leu Phe Pro Gly Ser Phe Val Glu Asn Ile
 885 890

<210> 10
 <211> 3149
 <212> DNA
 <213> Drosophila melanogaster

<400> 10
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 agcgattata atagtagatt ttagcatttg agctaaattt atttcccaac cgcgtcttgg 180
 gattgcgtat gcgtgagccca gtacctgc当地 gtgtgtgtgt tttggaatgtt ggcctgc当地 240
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 ttaaacgacc tggggaggatc ctccgtgtgt cttgagcgc当地 tggacaccac atcgaagggt 360
 ctgccatgcc accacaccc ttggccgcaaa tgcttgc当地 acattgtggc cagtcagcac 420
 aagttgc当地 gcccggaggatc cgc当地 ctgc当地 aaattgtatc gctgc当地 480
 aacgtcttgc ttagtgc当地 cttagaaggc atgaaaacaaa atgc当地 cgc当地 tggcaaagg 540
 gaagaaaagg gagaggagac tggaaacacag cc当地 gaaaggcccaaa acctca gccgccc当地 600
 gaatcagttgg ccccgcttgc当地 caaccaacta ctccagctgc当地 agtc当地 acatca gcaatctcat 660
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 caggtatgc gccc当地 gaggttgc当地 tcataattgg gc当地 agaggac gaattggc当地 gaccatcg 1020
 atcttccaa tagcattgc当地 tgagctgaat gc当地 agccggcccaaaa agctgtttt ggacagcggg 1080
 ctacacaccc atccattctg cc当地 atccaccc local aagcaacagg ggc当地 agccgggc ccttccctcc 1140
 gttccagttt ttgatccc当地 ggtggtcaag gaatc当地 caggatcc local caatccac 1200
 cc当地 gggc当地 gagca gcaatttcaag ctccacatcc local agctc当地 gaatac local cccac 1260
 attc当地 tactgc当地 cgaatcccccc ccaacatgtt当地 gtagcttccg gatc当地 cggc当地 gtc当地 tgttc当地 gtttcc 1320
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 cc当地 attaaggatc tgctgc当地 gagccat tc当地 ggctgaaa ttcttagctg ccccatgaa 1440
 ctaaggccct tggaaggttt cagctcaaca gctctaaaac cc当地 acgtc当地 cccacagaca 1500
 tc当地 cgtgtac ttaagaccac tggtc当地 gagc当地 cagatc当地 aac local ttacc ct当地 ggggatac 1560
 tt当地 agccctgt tcccatacaacc accacgccaa acggatgagc tggaattaaa aaagggtt 1620

gtttacattg tgaccgaacg atgtgtggac ggttgggtca agggaaaaaaa ctgggtggac 1680
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 gctagccatg taagacttag ggaacagttt cttaaaggcctt agcgattttt tagctagaga 3060
 aataatctaa ccgatcccttgc tggccctctac aaagtattt gtaatataacg atactcagta 3120
 ataaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 3149

<210> 11
 <211> 838
 <212> PRT
 <213> Drosophila melanogaster

<400> 11
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 20 25 30
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 35 40 45
 Cys Pro Glu Cys Arg Ile Leu Val Ser Cys Lys Ile Asp Glu Leu Pro
 50 55 60
 Pro Asn Val Leu Leu Met Arg Ile Leu Glu Gly Met Lys Gln Asn Ala
 65 70 75 80
 Ala Ala Gly Lys Gly Glu Glu Lys Gly Glu Glu Thr Glu Thr Gln Pro
 85 90 95
 Glu Arg Ala Lys Pro Gln Pro Pro Ala Glu Ser Val Ala Pro Pro Asp
 100 105 110
 Asn Gln Leu Leu Gln Leu Gln Ser His Gln Gln Ser His Gln Pro Ala
 115 120 125
 Arg His Lys Gln Arg Arg Phe Leu Leu Pro His Ala Tyr Ala Leu Phe
 130 135 140
 Asp Phe Ala Ser Gly Glu Ala Thr Asp Leu Lys Phe Lys Lys Gly Asp
 145 150 155 160
 Leu Ile Leu Ile Lys His Arg Ile Asp Asn Asn Trp Phe Val Gly Gln
 165 170 175
 Ala Asn Gly Gln Glu Gly Thr Phe Pro Ile Asn Tyr Val Lys Val Ser
 180 185 190
 Val Pro Leu Pro Met Pro Gln Cys Ile Ala Met Tyr Asp Phe Lys Met
 195 200 205

Gly Pro Asn Asp Glu Glu Gly Cys Leu Glu Phe Lys Lys Ser Thr Val
 210 215 220
 Ile Gln Val Met Arg Arg Val Asp His Asn Trp Ala Glu Gly Arg Ile
 225 230 235 240
 Gly Gln Thr Ile Gly Ile Phe Pro Ile Ala Phe Val Glu Leu Asn Ala
 245 250 255
 Ala Ala Lys Lys Leu Leu Asp Ser Gly Leu His Thr His Pro Phe Cys
 260 265 270
 His Pro Pro Lys Gln Gln Gly Gln Arg Ala Leu Pro Pro Val Pro Val
 275 280 285
 Ile Asp Pro Thr Val Val Thr Glu Ser Ser Ser Gly Ser Ser Asn Ser
 290 295 300
 Thr Pro Gly Ser Ser Asn Ser Ser Ser Thr Ser Ser Asn Asn Cys
 305 310 315 320
 Ser Pro Asn His Gln Ile Ser Leu Pro Asn Thr Pro Gln His Val Val
 325 330 335
 Ala Ser Gly Ser Ala Ser Val Arg Phe Arg Asp Lys Gly Ala Lys Glu
 340 345 350
 Lys Arg His Ser Leu Asn Ala Leu Leu Gly Gly Ala Pro Leu Ser
 355 360 365
 Leu Leu Gln Thr Asn Arg His Ser Ala Glu Ile Leu Ser Leu Pro His
 370 375 380
 Glu Leu Ser Arg Leu Glu Val Ser Ser Ser Thr Ala Leu Lys Pro Thr
 385 390 395 400
 Ser Ala Pro Gln Thr Ser Arg Val Leu Lys Thr Thr Val Gln Gln
 405 410 415
 Met Gln Pro Asn Leu Pro Trp Gly Tyr Leu Ala Leu Phe Pro Tyr Lys
 420 425 430
 Pro Arg Gln Thr Asp Glu Leu Glu Leu Lys Lys Gly Cys Val Tyr Ile
 435 440 445
 Val Thr Glu Arg Cys Val Asp Gly Trp Phe Lys Gly Lys Asn Trp Leu
 450 455 460
 Asp Ile Thr Gly Val Phe Pro Gly Asn Tyr Leu Thr Pro Leu Arg Ala
 465 470 475 480
 Arg Asp Gln Gln Leu Met His Gln Trp Lys Tyr Val Pro Gln Asn
 485 490 495
 Ala Asp Ala Gln Met Ala Gln Val Gln Gln His Pro Val Ala Pro Asp
 500 505 510
 Val Arg Leu Asn Asn Met Leu Ser Met Gln Pro Pro Asp Leu Pro Pro
 515 520 525
 Arg Gln Gln Gln Ala Thr Ala Thr Thr Thr Ser Cys Ser Val Trp Ser
 530 535 540
 Lys Pro Val Glu Ala Leu Phe Ser Arg Lys Ser Glu Pro Lys Pro Glu
 545 550 555 560
 Thr Ala Thr Ala Ser Thr Thr Ser Ser Ser Ser Gly Ala Val Gly
 565 570 575
 Leu Met Arg Arg Leu Thr His Met Lys Thr Arg Ser Lys Ser Pro Gly
 580 585 590
 Ala Ser Leu Gln Gln Val Pro Lys Glu Ala Ile Ser Thr Asn Val Glu
 595 600 605
 Phe Thr Thr Asn Pro Ser Ala Lys Leu His Pro Val His Val Arg Ser
 610 615 620
 Gly Ser Cys Pro Ser Gln Leu Gln His Ser Gln Pro Leu Asn Glu Thr
 625 630 635 640
 Pro Ala Ala Lys Thr Ala Ala Gln Gln Gln Phe Leu Pro Lys Gln
 645 650 655
 Leu Pro Ser Ala Ser Thr Asn Ser Val Ser Tyr Gly Ser Gln Arg Val
 660 665 670

Lys Gly Ser Lys Glu Arg Pro His Leu Ile Cys Ala Arg Gln Ser Leu
 675 680 685
 Asp Ala Ala Thr Phe Arg Ser Met Tyr Asn Asn Ala Ala Ser Pro Pro
 690 695 700
 Pro Pro Thr Thr Ser Val Ala Pro Ala Val Tyr Ala Gly Gly Gln Gln
 705 710 715 720
 Gln Val Ile Pro Gly Gly Ala Gln Ser Gln Leu His Ala Asn Met
 725 730 735
 Ile Ile Ala Pro Ser His Arg Lys Ser His Ser Leu Asp Ala Ser His
 740 745 750
 Val Leu Ser Pro Ser Ser Asn Met Ile Thr Glu Ala Ala Ile Lys Ala
 755 760 765
 Ser Ala Thr Thr Lys Ser Pro Tyr Cys Thr Arg Glu Ser Arg Phe Arg
 770 775 780
 Cys Ile Val Pro Tyr Pro Pro Asn Ser Asp Ile Glu Leu Glu Leu His
 785 790 795 800
 Leu Gly Asp Ile Ile Tyr Val Gln Arg Lys Gln Lys Asn Gly Trp Tyr
 805 810 815
 Lys Gly Thr His Ala Arg Thr His Lys Thr Gly Leu Phe Pro Ala Ser
 820 825 830
 Phe Val Glu Pro Asp Cys
 835

<210> 12
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 12
 cttgccttgc cagcatac
 <210> 13
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 13
 ctgccagcat tccttcag
 <210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> target sequence

<400> 14
 aacagaggcc ttggaaacct g

<210> 15
 <211> 21

18

18

21

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<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 15
ttcagaggcc uuggaaaccu g                                21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 16
ttcagguuuc caaggccucu g                                21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> target sequence

<400> 17
aaagagcctg gagacacctaa a                                21

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 18
ttagagccug gagaccuuua a                                21

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 19
ttuuaagggu cuccaggcuc u                                21

<210> 20
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<212> DNA
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<220>

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<223> target sequence

<400> 20
aaggatttgtt atgtgactct g 21

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 21
ttggauuggu augugacucu g 21

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 22
ttcagaguca cauaccaauc c 21

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> target sequence

<400> 23
aagctggatt atctccctgtt g 21

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 24
ttgcuggauu aucuccuguu g 21

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 25
ttcaacagga gauaauccag c 21

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<210> 26

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> RING domain

<400> 26

Cys	Pro	Val	Cys	Leu	Glu	Arg	Leu	Asp	Ala	Ser	Ala	Lys	Val	Leu	Pro
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Cys	Gln	His	Thr	Phe	Cys	Lys	Arg	Cys	Leu	Leu	Gly	Ile	Val	Gly	Ser
	20					25						30			
Arg	Asn	Glu	Leu	Arg	Cys	Pro	Glu	Cys							
	35					40									

<210> 27

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 domain

<400> 27

Pro	Cys	Ala	Lys	Ala	Leu	Tyr	Asn	Tyr	Glu	Gly	Lys	Glu	Pro	Gly	Asp
1				5					10				15		
Leu	Lys	Phe	Ser	Lys	Gly	Asp	Ile	Ile	Ile	Leu	Arg	Arg	Gln	Val	Asp
	20					25				30					
Glu	Asn	Trp	Tyr	His	Gly	Glu	Val	Asn	Gly	Ile	His	Gly	Phe	Phe	Pro
	35					40				45					
Thr	Asn	Phe	Val	Gln	Ile	Ile	Lys								
	50					55									

<210> 28

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 domain

<400> 28

Pro	Gln	Cys	Lys	Ala	Leu	Tyr	Asp	Phe	Glu	Val	Lys	Asp	Lys	Glu	Ala
1				5					10				15		
Asp	Lys	Asp	Cys	Leu	Pro	Phe	Ala	Lys	Asp	Asp	Val	Leu	Thr	Val	Ile
	20						25					30			
Arg	Arg	Val	Asp	Glu	Asn	Trp	Ala	Glu	Gly	Met	Leu	Ala	Asp	Lys	Ile
	35						40				45				
Gly	Ile	Phe	Pro	Ile	Ser	Tyr	Val	Glu	Phe	Asn	Ser				
	50					55				60					

<210> 29

<211> 58

<212> PRT

<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 29
Ser Val Tyr Val Ala Ile Tyr Pro Tyr Thr Pro Arg Lys Glu Asp Glu
1 5 10 15
Leu Glu Leu Arg Lys Gly Glu Met Phe Leu Val Phe Glu Arg Cys Gln
20 25 30
Asp Gly Trp Phe Lys Gly Thr Ser Met His Thr Ser Lys Ile Gly Val
35 40 45
Phe Pro Gly Asn Tyr Val Ala Pro Val Thr
50 55

<210> 30
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 30
Glu Arg His Arg Val Val Val Ser Tyr Pro Pro Gln Ser Glu Ala Glu
1 5 10 15
Leu Glu Leu Lys Glu Gly Asp Ile Val Phe Val His Lys Lys Arg Glu
20 25 30
Asp Gly Trp Phe Lys Gly Thr Leu Gln Arg Asn Gly Lys Thr Gly Leu
35 40 45
Phe Pro Gly Ser Phe Val Glu Asn Ile
50 55

<210> 31
<211> 121
<212> DNA
<213> Artificial Sequence

<220>
<223> RING domain

<400> 31
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ttttgcaagc gatgttgct ggggatcgta ggttctcgaa atgaaactcgat atgtcccggag 120
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<210> 32
<211> 165
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 32
ccatgtgccaa aagcgttata caactatgaa ggaaaaagagc ctggagaccc taaaattcagc 60
aaaggcgaca tcatcatttt gccaagacaa gtggatgaaa attggatcca tggggaaatgc 120
aatggaatcc atggctttt cccccaccaac tttgtgcaga ttatt 165

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<210> 33
<211> 177
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 33
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cttccatgg caaaggatga tggatcgact gtcgtccgaa gagtggatga aaactggct 120
gaaggaatgc tggcagacaa aataggaata ttccaattt catatgttga gtttaac 177

<210> 34
<211> 171
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 34
agtgtgtatg ttgcttatata tccatacact cctcgaaaag aggatgaact agagctgaga 60
aaaggggaga tggatcgact gtttgagcgc tgccaggatg gctggttcaa agggacatcc 120
atgcatacca gcaagatagg gttttccct ggcaattatg tggcaccagt c 171

<210> 35
<211> 169
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 35
gaaaggcaca ggggtgggtt ttcctatcct cctcagatg aggccagaact tgaactaaa 60
gaaggagata ttgtgttgt tcataaaaaa cgagaggatg gctggttcaa aggcacatta 120
caacgtaatg gaaaaactgg cttttccca ggaagcttg tggaaaaca 169

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> target sequence

<400> 36
aagtccaaag gttccggaga c 21

<210> 37
<211> 4
<212> PRT
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<220>
<223> chemically synthesized

<220>

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<221> VARIANT
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<223> Xaa = Thr or Ser

<400> 37
Pro Xaa Ala Pro
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<210> 38
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 38
Pro Phe Arg Asp Tyr
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 39
Arg Pro Glu Pro Thr Ala Pro
1 5

<210> 40
<211> 7
<212> PRT
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<220>
<223> chemically synthesized

<400> 40
Arg Gln Gly Pro Lys Glu Pro
1 5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 41
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1 5

<210> 42

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> chemically synthesized

<400> 42

Arg Pro Glu Pro Thr Ala Pro Glu Glu
1 5

<210> 43

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> chemically synthesized

<400> 43

Arg Pro Leu Pro Val Ala Pro
1 5

<210> 44

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> scrambled human POSH oligonucleotide

<400> 44

cacacactgc cgtcaactgt tcaagagaca gttgacggca gtgtgtgttt ttt 53

<210> 45

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> scrambled human POSH oligonucleotide

<400> 45

aattaaaaaaaa cacacactgc cgtcaactgt ctcttgaaca gttgacggca gtgtgtgggc 60
c 61

<210> 46

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide encoding RNAi against human POSH

<400> 46

aacagaggcc ttggaaacct ggaagcttgc aggtttccaa ggctctgtt 50

<210> 47
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide encoding RNAi against human POSH

<400> 47
gatcaacaga ggcttgaa acctgcaagc ttccaggttt ccaaggcctc tgtt 54

<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48
ggcccaactag tcaaggctcg gcaggaaga 29

<210> 49
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
gccgaattca aaaaggatcc ggcgatatcc ggtgttcgt cctttcca 48

<210> 50
<211> 836
<212> PRT
<213> Artificial Sequence

<220>
<223> POSH fragment

<400> 50
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20 25 30
Pro Gly Gly Ser Gly Thr Asn Cys Thr Asn Ala Leu Arg Ser Gln
35 40 45
Ser Ser Thr Val Ala Asn Cys Ser Ser Lys Asp Leu Gln Ser Ser Gln
50 55 60
Gly Gly Gln Gln Pro Arg Val Gln Ser Trp Ser Pro Pro Val Arg Gly
65 70 75 80
Ile Pro Gln Leu Pro Cys Ala Lys Ala Leu Tyr Asn Tyr Glu Gly Lys
85 90 95
Glu Pro Gly Asp Leu Lys Phe Ser Lys Gly Asp Ile Ile Ile Leu Arg
100 105 110

Arg Gln Val Asp Glu Asn Trp Tyr His Gly Glu Val Asn Gly Ile His
 115 120 125
 Gly Phe Phe Pro Thr Asn Phe Val Gln Ile Ile Lys Pro Leu Pro Gln
 130 135 140
 Pro Pro Pro Gln Cys Lys Ala Leu Tyr Asp Phe Glu Val Lys Asp Lys
 145 150 155 160
 Glu Ala Asp Lys Asp Cys Leu Pro Phe Ala Lys Asp Asp Val Leu Thr
 165 170 175
 Val Ile Arg Arg Val Asp Glu Asn Trp Ala Glu Gly Met Leu Ala Asp
 180 185 190
 Lys Ile Gly Ile Phe Pro Ile Ser Tyr Val Glu Phe Asn Ser Ala Ala
 195 200 205
 Lys Gln Leu Ile Glu Trp Asp Lys Pro Pro Val Pro Gly Val Asp Ala
 210 215 220
 Gly Glu Cys Ser Ser Ala Ala Ala Gln Ser Ser Thr Ala Pro Lys His
 225 230 235 240
 Ser Asp Thr Lys Lys Asn Thr Lys Lys Arg His Ser Phe Thr Ser Leu
 245 250 255
 Thr Met Ala Asn Lys Ser Ser Gln Ala Ser Gln Asn Arg His Ser Met
 260 265 270
 Glu Ile Ser Pro Pro Val Leu Ile Ser Ser Asn Pro Thr Ala Ala
 275 280 285
 Ala Arg Ile Ser Glu Leu Ser Gly Leu Ser Cys Ser Ala Pro Ser Gln
 290 295 300
 Val His Ile Ser Thr Thr Gly Leu Ile Val Thr Pro Pro Pro Ser Ser
 305 310 315 320
 Pro Val Thr Thr Gly Pro Ser Phe Thr Phe Pro Ser Asp Val Pro Tyr
 325 330 335
 Gln Ala Ala Leu Gly Thr Leu Asn Pro Pro Leu Pro Pro Pro Leu
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 Leu Ala Ala Thr Val Leu Ala Ser Thr Pro Pro Gly Ala Thr Ala Ala
 355 360 365
 Ala Ala Ala Ala Gly Met Gly Pro Arg Pro Met Ala Gly Ser Thr Asp
 370 375 380
 Gln Ile Ala His Leu Arg Pro Gln Thr Arg Pro Ser Val Tyr Val Ala
 385 390 395 400
 Ile Tyr Pro Tyr Thr Pro Arg Lys Glu Asp Glu Leu Glu Leu Arg Lys
 405 410 415
 Gly Glu Met Phe Leu Val Phe Glu Arg Cys Gln Asp Gly Trp Phe Lys
 420 425 430
 Gly Thr Ser Met His Thr Ser Lys Ile Gly Val Phe Pro Gly Asn Tyr
 435 440 445
 Val Ala Pro Val Thr Arg Ala Val Thr Asn Ala Ser Gln Ala Lys Val
 450 455 460
 Pro Met Ser Thr Ala Gly Gln Thr Ser Arg Gly Val Thr Met Val Ser
 465 470 475 480
 Pro Ser Thr Ala Gly Gly Pro Ala Gln Lys Leu Gln Gly Asn Gly Val
 485 490 495
 Ala Gly Ser Pro Ser Val Val Pro Ala Ala Val Val Ser Ala Ala His
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 Ile Gln Thr Ser Pro Gln Ala Lys Val Leu Leu His Met Thr Gly Gln
 515 520 525
 Met Thr Val Asn Gln Ala Arg Asn Ala Val Arg Thr Val Ala Ala His
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 Asn Gln Glu Arg Pro Thr Ala Ala Val Thr Pro Ile Gln Val Gln Asn
 545 550 555 560
 Ala Ala Gly Leu Ser Pro Ala Ser Val Gly Leu Ser His His Ser Leu
 565 570 575

Ala Ser Pro Gln Pro Ala Pro Leu Met Pro Gly Ser Ala Thr His Thr
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 Ala Ala Ile Ser Ile Ser Arg Ala Ser Ala Pro Leu Ala Cys Ala Ala
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 Ala Ala Pro Leu Thr Ser Pro Ser Ile Thr Ser Ala Ser Leu Glu Ala
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 625 630 635 640
 Pro Asp Ser Ala Ser Ser Ala Cys Gly Asn Ser Ser Ala Thr Lys Pro
 645 650 655
 Asp Lys Asp Ser Lys Lys Glu Lys Lys Gly Leu Leu Lys Leu Leu Ser
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 Gly Ala Ser Thr Lys Arg Lys Pro Arg Val Ser Pro Pro Ala Ser Pro
 675 680 685
 Thr Leu Glu Val Glu Leu Gly Ser Ala Glu Leu Pro Leu Gln Gly Ala
 690 695 700
 Val Gly Pro Glu Leu Pro Pro Gly Gly His Gly Arg Ala Gly Ser
 705 710 715 720
 Cys Pro Val Asp Gly Asp Gly Pro Val Thr Thr Ala Val Ala Gly Ala
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 Ala Leu Ala Gln Asp Ala Phe His Arg Lys Ala Ser Ser Leu Asp Ser
 740 745 750
 Ala Val Pro Ile Ala Pro Pro Pro Arg Gln Ala Cys Ser Ser Leu Gly
 755 760 765
 Pro Val Leu Asn Glu Ser Arg Pro Val Val Cys Glu Arg His Arg Val
 770 775 780
 Val Val Ser Tyr Pro Pro Gln Ser Glu Ala Glu Leu Glu Leu Lys Glu
 785 790 795 800
 Gly Asp Ile Val Phe Val His Lys Lys Arg Glu Asp Gly Trp Phe Lys
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 <213> Homo sapiens

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<210> 52

<211> 2217

<212> DNA

<213> Homo sapiens

<400> 52

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<210> 53

<211> 1684

<212> DNA

<213> Homo sapiens

<400> 53

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<400> 54

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<210> 55

<211> 1864

<212> DNA

<213> Homo sapiens

<400> 55

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<210> 56

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 56

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<210> 57
 <211> 1865
 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58
<211> 1884
<212> DNA
<213> Homo sapiens

<400> 58

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cgcgtccaga	ggaccagagg	ttaattttt	ctggaaagct	gttgggttat	caccaatgtc	300
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<210> 59
<211> 1860
<212> DNA
<213> Homo sapiens

<400> 59

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<210> 60
<211> 1884
<212> DNA
<213> Homo sapiens

<400> 60
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<210> 61
<211> 232
<212> PRT
<213> Homo sapiens

<400> 61
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 20 25 30
 Ser Val Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
 35 40 45
 Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
 50 55 60
 Asp His Gln Cys Leu Arg Asp Leu Leu Pro Lys Glu Lys Arg His Val
 65 70 75 80
 Leu His Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu Ile
 85 90 95
 Asn Ala Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg
 100 105 110
 Gly Gln Tyr Pro Glu Asp Ser Ser Asp Gly Leu Arg Gln Arg Glu
 115 120 125
 Val Leu Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg His
 130 135 140
 His Val Gly Trp Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro
 145 150 155 160
 Asn Asp Gly Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn
 165 170 175
 Leu Gln Glu Gly Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro
 180 185 190
 Pro Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met
 195 200 205
 Ser Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro
 210 215 220
 Glu Gly Pro Pro Ala Ile Ala Asn
 225 230

<210> 62
<211> 209
<212> PRT
<213> Homo sapiens

<400> 62
 Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe Val Pro Pro
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 Pro Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala Pro Ala Pro
 20 25 30
 Ile His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn Gln Asn Ala
 35 40 45

Ala Pro Gln Val Val Val Asn Pro Gly Ala Asn Gln Asn Leu Arg Met
 50 55 60
 Asn Ala Gln Gly Gly Pro Ile Val Glu Glu Asp Asp Glu Ile Asn Arg
 65 70 75 80
 Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala Thr Phe Ser Val Phe Leu
 85 90 95
 Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser Arg Phe Leu Met Val Met
 100 105 110
 Gly Ala Thr Val Val Met Tyr Leu His His Val Gly Trp Phe Pro Phe
 115 120 125
 Arg Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro Pro Pro Asp
 130 135 140
 Val Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly Thr Asp Pro
 145 150 155 160
 Glu Thr Glu Asp Pro Asn His Leu Pro Pro Asp Arg Asp Val Leu Asp
 165 170 175
 Gly Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp Leu Val Phe
 180 185 190
 Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu Gly Pro Pro Ala Ile Ala
 195 200 205
 Asn

<210> 63
 <211> 356
 <212> PRT
 <213> Homo sapiens

<400> 63
 Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg Pro Arg
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 Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu Asp His
 20 25 30
 Gln Cys Leu Arg Asp Leu Leu Pro Lys Glu Lys Arg His Val Leu His
 35 40 45
 Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu Ile Asn Ala
 50 55 60
 Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg Gly Gln
 65 70 75 80
 Tyr Pro Glu Asp Ser Ser Asp Gly Leu Arg Gln Arg Glu Val Leu
 85 90 95
 Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg Pro Glu Ala
 100 105 110
 Ala Gln Gln Ala Phe Gln Gly Leu Gly Pro Gly Phe Ser Gly Tyr Thr
 115 120 125
 Pro Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile Tyr Ala Arg
 130 135 140
 Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe
 145 150 155 160
 Val Pro Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala
 165 170 175
 Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn
 180 185 190
 Gln Asn Ala Ala Pro Gln Val Val Asn Pro Gly Ala Asn Gln Asn
 195 200 205
 Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu Asp Asp Glu
 210 215 220

Ile	Asn	Arg	Asp	Trp	Leu	Asp	Trp	Thr	Tyr	Ser	Ala	Ala	Thr	Phe	Ser
225				230					235					240	
Val	Phe	Leu	Ser	Ile	Leu	Tyr	Phe	Tyr	Ser	Ser	Leu	Ser	Arg	Phe	Leu
	245								250					255	
Met	Val	Met	Gly	Ala	Thr	Val	Val	Met	Tyr	Leu	His	His	Val	Gly	Trp
	260							265					270		
Phe	Pro	Phe	Arg	Pro	Arg	Pro	Val	Gln	Asn	Phe	Pro	Asn	Asp	Gly	Pro
	275						280					285			
Pro	Pro	Asp	Val	Val	Asn	Gln	Asp	Pro	Asn	Asn	Asn	Leu	Gln	Glu	Gly
	290				295							300			
Thr	Asp	Pro	Glu	Thr	Glu	Asp	Pro	Asn	His	Leu	Pro	Pro	Asp	Arg	Asp
305				310						315				320	
Val	Leu	Asp	Gly	Glu	Gln	Thr	Ser	Pro	Ser	Phe	Met	Ser	Thr	Ala	Trp
		325							330				335		
Leu	Val	Phe	Lys	Thr	Phe	Phe	Ala	Ser	Leu	Leu	Pro	Glu	Gly	Pro	Pro
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<210> 64
<211> 391
<212> PRT
<213> Homo sapiens

<400> 64															
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Ser	Val	Gly	His	Leu	Lys	Ala	His	Leu	Ser	Arg	Val	Tyr	Pro	Glu	Arg
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Pro	Arg	Pro	Glu	Asp	Gln	Arg	Leu	Ile	Tyr	Ser	Gly	Lys	Leu	Leu	Leu
				50				55				60			
Asp	His	Gln	Cys	Leu	Arg	Asp	Leu	Leu	Pro	Lys	Gln	Glu	Lys	Arg	His
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Val	Leu	His	Leu	Val	Cys	Asn	Val	Lys	Ser	Pro	Ser	Lys	Met	Pro	Glu
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Ile	Asn	Ala	Lys	Val	Ala	Glu	Ser	Thr	Glu	Glu	Pro	Ala	Gly	Ser	Asn
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Arg	Gly	Gln	Tyr	Pro	Glu	Asp	Ser	Ser	Ser	Asp	Gly	Leu	Arg	Gln	Arg
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Glu	Val	Leu	Arg	Asn	Leu	Ser	Ser	Pro	Gly	Trp	Glu	Asn	Ile	Ser	Arg
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Pro	Glu	Ala	Ala	Gln	Gln	Ala	Phe	Gln	Gly	Leu	Gly	Pro	Gly	Phe	Ser
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					165				170				175		
Tyr	Ala	Arg	Gln	Tyr	Tyr	Met	Gln	Tyr	Leu	Ala	Ala	Thr	Ala	Ala	Ser
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Gly	Ala	Phe	Val	Pro	Pro	Pro	Ser	Ala	Gln	Glu	Ile	Pro	Val	Val	Ser
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Ala	Pro	Ala	Pro	Ala	Pro	Ile	His	Asn	Gln	Phe	Pro	Ala	Glu	Asn	Gln
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Pro	Ala	Asn	Gln	Asn	Ala	Ala	Pro	Gln	Val	Val	Val	Asn	Pro	Gly	Ala
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Asn	Gln	Asn	Leu	Arg	Met	Asn	Ala	Gln	Gly	Gly	Pro	Ile	Val	Glu	Glu
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Asp	Asp	Glu	Ile	Asn	Arg	Asp	Trp	Leu	Asp	Trp	Thr	Tyr	Ser	Ala	Ala
260							265						270		
Thr	Phe	Ser	Val	Phe	Leu	Ser	Ile	Leu	Tyr	Phe	Tyr	Ser	Ser	Leu	Ser
275							280						285		
Arg	Phe	Leu	Met	Val	Met	Gly	Ala	Thr	Val	Val	Met	Tyr	Leu	His	His
290						295					300				
Val	Gly	Trp	Phe	Pro	Phe	Arg	Pro	Arg	Pro	Val	Gln	Asn	Phe	Pro	Asn
305						310				315			320		
Asp	Gly	Pro	Pro	Asp	Val	Val	Asn	Gln	Asp	Pro	Asn	Asn	Asn	Leu	
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Gln	Glu	Gly	Thr	Asp	Pro	Glu	Thr	Glu	Asp	Pro	Asn	His	Leu	Pro	Pro
							340			345			350		
Asp	Arg	Asp	Val	Leu	Asp	Gly	Glu	Gln	Thr	Ser	Pro	Ser	Phe	Met	Ser
							355			360			365		
Thr	Ala	Trp	Leu	Val	Phe	Lys	Thr	Phe	Phe	Ala	Ser	Leu	Leu	Pro	Glu
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						385									
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<210> 65
<211> 1857
<212> DNA
<213> Rat

<400> 65
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tcattgtttt ttaaaaacgca gtgttactt actgaggggcg gcgacttggc acaggtaaag 1800
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<210> 66

<211> 391
<212> PRT
<213> Rat

<400> 66
Met Glu Pro Glu Pro Gln Pro Glu Pro Val Thr Leu Leu Val Lys Ser
1 5 10 15
Pro Asn Gln Arg His Arg Asp Leu Glu Leu Ser Gly Asp Arg Gly Trp
20 25 30
Ser Val Ser Arg Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
35 40 45
Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
50 55 60
Asp His Gln Cys Leu Gln Asp Leu Leu Pro Lys Gln Glu Lys Arg His
65 70 75 80
Val Leu His Leu Val Cys Asn Val Arg Ser Pro Ser Lys Lys Pro Glu
85 90 95
Ala Ser Thr Lys Gly Ala Glu Ser Thr Glu Gln Pro Asp Asn Thr Ser
100 105 110
Gln Ala Gln Tyr Pro Gly Asp Ser Ser Ser Asp Gly Leu Arg Glu Arg
115 120 125
Glu Val Leu Arg Asn Leu Pro Pro Ser Gly Trp Glu Asn Val Ser Arg
130 135 140
Pro Glu Ala Val Gln Gln Thr Phe Gln Gly Leu Gly Pro Gly Phe Ser
145 150 155 160
Gly Tyr Thr Thr Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
165 170 175
Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser
180 185 190
Gly Ala Phe Gly Pro Thr Pro Ser Ala Gln Glu Ile Pro Val Val Ser
195 200 205
Thr Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln
210 215 220
Pro Ala Asn Gln Asn Ala Ala Ala Gln Ala Val Val Asn Pro Gly Ala
225 230 235 240
Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Leu Val Glu Glu
245 250 255
Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala
260 265 270
Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser
275 280 285
Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His
290 295 300
Val Gly Trp Phe Pro Phe Arg Gln Arg Pro Val Gln Asn Phe Pro Asp
305 310 315 320
Asp Gly Pro Pro Gln Glu Ala Ala Asn Gln Asp Pro Asn Asn Asn Leu
325 330 335
Gln Gly Gly Leu Asp Pro Glu Met Glu Asp Pro Asn Arg Leu Pro Val
340 345 350
Gly Arg Glu Val Leu Asp Pro Glu His Thr Ser Pro Ser Phe Met Ser
355 360 365
Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu
370 375 380
Gly Pro Pro Ala Leu Ala Asn
385 390

<210> 67
<211> 1871

<212> DNA
<213> Mouse

<400> 67

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gcagttggag	tgtgagtcgc	ctcaaggccc	acctgagccg	agtctacccc	gagcgcggc	240
gtccagagga	ccagaggtta	atttattctg	ggaagctgct	gttggatcac	cagtgtctcc	300
aagatttgc	tccaaagcag	gaaaagcgcac	atgttttgc	ccttgtgtgc	aatgtgaaga	360
atccctccaa	aatgccagaa	accagcacaa	agggtgctga	atccacagag	cagccgacac	420
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tccccccaga	ccgcgaagt	ctggaccctg	agcacacccag	cccctcg	atgagcacag	1200
catggctagt	cttcaagact	ttcttgcct	cttttcttcc	agaaggccca	ccagccctag	1260
ccaactgtat	gcccttgc	tctgtcgctg	gtggctttga	cagctcgac	tggatcgct	1320
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ctgaacacagg	ccctcatgt	cgttattctg	aagagcttta	atgtatactg	tatgttagtt	1500
cataggcact	gtaagcagaa	ggcccagggt	cgcattttct	gcctgagcac	ctccccagat	1560
gtgtgtgc	gtgtgtgt	catggaaagtc	atagacgtgt	gtgcatgtgt	gctctacatg	1620
gaagtcata	atgcagaaac	ggttctgctg	gttcgatttg	attctgttg	aatgttcaa	1680
attacactaa	gtgtactact	ttatataatc	agtgaattgc	tagacatgtt	agcaggactt	1740
ttcttaggaga	gacttatgt	taattgc	ttaaaatgca	gtgc	ttaaaaccgag	1800
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<210> 68

<211> 391

<212> PRT

<213> Mouse

<400> 68

Met	Glu	Pro	Glu	Pro	Gln	Pro	Glu	Pro	Val	Thr	Leu	Leu	Val	Lys	Ser
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Pro	Asn	Gln	Arg	His	Arg	Asp	Leu	Glu	Leu	Ser	Gly	Asp	Arg	Ser	Trp
					20				25				30		
Ser	Val	Ser	Arg	Leu	Lys	Ala	His	Leu	Ser	Arg	Val	Tyr	Pro	Glu	Arg
					35				40				45		
Pro	Arg	Pro	Glu	Asp	Gln	Arg	Leu	Ile	Tyr	Ser	Gly	Lys	Leu	Leu	Leu
					50			55				60			
Asp	His	Gln	Cys	Leu	Gln	Asp	Leu	Leu	Pro	Lys	Gln	Glu	Lys	Arg	His
					65			70			75			80	
Val	Leu	His	Leu	Val	Cys	Asn	Val	Lys	Asn	Pro	Ser	Lys	Met	Pro	Glu
					85				90				95		
Thr	Ser	Thr	Lys	Gly	Ala	Glu	Ser	Thr	Glu	Gln	Pro	Asp	Asn	Ser	Asn
					100				105				110		
Gln	Thr	Gln	His	Pro	Gly	Asp	Ser	Ser	Ser	Asp	Gly	Leu	Arg	Gln	Arg
					115				120				125		

Glu Val Leu Arg Asn Leu Ser Pro Ser Gly Trp Glu Asn Ile Ser Arg
 130 135 140
 Pro Glu Ala Val Gln Gln Thr Phe Gln Gly Leu Gly Pro Gly Phe Ser
 145 150 155 160
 Gly Tyr Thr Thr Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
 165 170 175
 Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser
 180 185 190
 Gly Thr Phe Val Pro Thr Pro Ser Ala Gln Glu Ile Pro Val Val Ser
 195 200 205
 Thr Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln
 210 215 220
 Pro Ala Asn Gln Asn Ala Ala Ala Gln Ala Val Val Asn Pro Gly Ala
 225 230 235 240
 Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Leu Val Glu Glu
 245 250 255
 Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala
 260 265 270
 Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser
 275 280 285
 Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His
 290 295 300
 Val Gly Trp Phe Pro Phe Arg Gln Arg Pro Val Gln Asn Phe Pro Asp
 305 310 315 320
 Asp Gly Gly Pro Arg Asp Ala Ala Asn Gln Asp Pro Asn Asn Asn Leu
 325 330 335
 Gln Gly Gly Met Asp Pro Glu Met Glu Asp Pro Asn Arg Leu Pro Pro
 340 345 350
 Asp Arg Glu Val Leu Asp Pro Glu His Thr Ser Pro Ser Phe Met Ser
 355 360 365
 Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu
 370 375 380
 Gly Pro Pro Ala Leu Ala Asn
 385 390

<210> 69
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA

<400> 69
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21

<210> 70
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA

<400> 70
 ttcccucaa gaagccuagg a

21